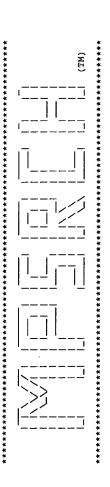
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Jul 22 15:27:41 1998; MasPar time 12.38 Seconds 767.369 Million cell updates/sec

Tabular output not generated.

>US-08-915-659A-7 (1-260) from US08915659A.pep 1943 1 MGRPRPRAAKTWMFLLLLGG.......VYTNICRYLDWIKKIIGSKG 260

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 42.128; Variance 70.703; scale 0.596 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		e (
	Score	Match	Query Match Length DB	8	Ω	Description	Pred. No.
_	1488	76.6	260	7	156559	neuropsin - mouse	0.00e+00
. 4	833	42.9	253	~	A53968	serine proteinase SCC	3.84e-170
14)	808	41.6	247	Н	TRDG	trypsin (EC 3.4.21.4)	5.44e-164
4	1 804	41.4	238	7	S31779		5.23e-163
u,	5 795	40.9	246	Н	TRDGC	trypsin (EC 3.4.21.4)	8.52e-161
.	5 785	40.4	229	٦	TRBOTR	trypsin (EC 3.4.21.4)	2.43e-158
-	7 783	40.3	247	~	A27547	trypsin (EC 3.4.21.4)	7.53e-158
w	3 781	40.2	246	H	TRRT2	trypsin (EC 3.4.21.4)	2.33e-157
Ji		40.1	225	ß	1TGSZ	trypsin (EC 3.4.21.4)	7.22e-157
10		39.5	223	ທ	2TLDE	trypsin (EC 3.4.21.4)	3.60e-154
1	1 768	39.5	246	~	B25528	trypsin (EC 3.4.21.4)	3.60e-154
17	2 767	39.5	246	~	TRR11	trypsin (EC 3.4.21.4)	6.33e-154
H	3 766	39.4	223	Ŋ	1TPS	_	1.11e-153
14	1 766	39.4	223	S	ltyn	➣	1.11e-153
ï	992 9	39.4	223	ß	1JRTA	ന	1.11e-153
1	992 9	39.4	223	ហ	1JRSA	trypsin (EC 3.4.21.4)	1.11e - 153
Ä		39.4	223	'n	1TGB	trypsin (EC 3.4.21.4)	1.11e-153
ĭ		39.4	223	Ŋ	1TGT	trypsin (EC 3.4.21.4)	1.11e-153
13		39.4	223	Ŋ	4TPIZ	trypsin (EC 3.4.21.4)	1.11e-153
ř		39.4	223	Ŋ	2PTN	trypsin (EC 3.4.21.4)	1.11e-153
5	1 766	39.4	223	'n	1TPP	trypsin (EC 3.4.21.4)	1.11e-153
27	992 2	39.4	223	'n	1TPO	trypsin (EC 3.4.21.4)	1.11e-153
2	3 766	39.4	223	'n	1BTY	beta-trypsin (EC 3.4.	1.11e-153

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156559 #type complete neuropsin - mouse #formal_name Mus musculus #common_name house mouse 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 156559	Chey, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, Ananaka, T.; Ito, J.; Nishino, H.; Aimoto, S.; Kiyama,	vel					448	900		icee	TCGG	HSHD	HNHD	KIYS	KIFP	EKPG	DKPG	
mous text_	.; Su S.; K	a novel		9.7		н	9 mns	50;	ò	GERL	3000	SNPED	SDVED	NCAEV	NCAEV	PCGKP	PCGRS	
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lnence se se	ida,	J. Neurosci. (1995) 15:5088-5097 Expression and activity-dependent changes of limbic-serine protease qene in the hippocan	7.	##status preliminary; translated from GB/EMBL/DDBJ	R	##cross-references GB:D30785; NID:g1020090; PID:g1020091 FICATION #superfamily trypsin; trypsin homology E	#domain trypsin homology #label TRY #length 260 #molecular-weight 28523 #c	Score Pred	2	MGRPPPCAIQPWILLLLEWGAWAGLTRAQGSKILEGRECIPHSQFWQAALFQGERLICGG	GHSR/	VLVGDRWVLTAAAHCKKQKXSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSNPEDHSHD	GDHS	IMLIRLQNSANLGDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENPPNTLNCAEVKIYS	энсто	QNKCERAY PGKITEGMYCAGSSNGADTCQGDSGGPLYCDGMLQGITSWGSDPCGKPEKPG	GADT	
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1-247 ##label PIN

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#journal Mol. Cell. Biol. (1985) 5:2669-2676
#title Differential regulation of trypsinogen mRNA translation:
full.length mRNA sequences encoding two oppositely charged
#cross-references MUID:86284628
#accession A26273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 ENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQPNDPGVYTQVCKFTKW 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trypsin (EC 3.4.21.4) precursor, anionic - dog cationic trypsinogen #formal_name Canis lupus familiaris #common_name dog 30.5ep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jul-1997
                                                                                            #formal_name Homo sapiens #common_name man
07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change
08-Sep-1997
                                                                                                                                                                             Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt,
Carlstein, A.; Egelrud, T.
J. Biol. Chem. (1994) 269:19420-19426
Cloning, expression, and characterization of stratum conchymotryptic enzyme. A skin-specific human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain trypsin homology #label TRY
th 253 #molecular-weight 27525 #checksum 644
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Pred. No. 3.84e-170;
44; Mismatches 77; Indels
                                             A53968 #type complete
serine proteinase SCCE precursor · human
stratum corneum chymotryptic enzyme
                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GDB:377730
#map_position 7q35-7q35
CLASSIFICATION #superfamily trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                1-253 ##label HAN
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                                                                                                                                                                                                                                                                                             ##status preliminary ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.9%;
Best Local Similarity 47.3%;
Matches 116; Conservative
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#label Sic\
#domain activation peptide #status predicted #label APT\
#product trypsin III #status predicted #label MAT\
#domain trypsin homology #label TRY.
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#domain activation peptide #status predicted #label APT\
#product tryppin, anionic #status predicted #label ENZ\
#domain trypsin homology #label TRY.
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*superfamily trypsin; trypsin homology
hydrolase; pancreas; protein digestion; serine proteinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 TENMICAGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGYG-CAQKNKPGVYTKVCNFVDW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 HCYKSRIQVRLGEYNIDVLEGNEQFINSAKVIRHPNYNSW-ILD-N-DIMLIKLSSPAVL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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#active_site His, Asp, Ser #status predicted\
#binding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 247 #molecular-weight 26423 #checksum 8431
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22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change
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trypsin (EC 3.4.21.4) III precursor - Atlantic salmon
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    #active_site His, Asp, Ser #status predicted
#length 238 #checksum 6737
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Eur. J. Biochem. (1995) 232:677-685
Molecular cloning and characterization of anionic
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 247;
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Pred. No. 5.44e-164;
...matches 75; Indels
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44.28;
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S66657; S31779
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30-160,48-64,
132-233,139-206,
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16-238
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22-152,40-56,
124-225,131-198,
163-177,188-212
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                                                                                                                                                           TITLE
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#domain activation peptide #status predicted #label APT\
#product trypsin, cationic #status predicted #label ENZ\
#domain trypsin homology #label TRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Pinsky, S.D.; LaForge, K.S.; Scheele, G.
#journal Mol. Cell. Biol. (1985) 5:2669-2676
#title Differential regulation of trypsinogen mRNA translation:
full-length mRNA sequences encoding two oppositely charged
trypsinogen isoenzymes in the dog pancreas.
#cross-references MUID:86284628
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *superfamily trypsin; trypsin homology hydrolase; pancreas; protein digestion; serine proteinase;
                                                                                                                                                           SAAHCYKSRIQVRLGEYNIAVSEGGEQFINAAKIIRHPRYNANTI-D-N-DIMLIKLSSP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LPSSCASSGTRCLVSGWGNLSGSSSNYPDTLRCLDLPILSSSSCNSAYPGQITSNMFCAG 179
                                                                                                                                                                                                                                               141 LADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
                                                                                                                                                                                                                                                                                180 FMEGGKDSCQGDSGGPVVCNGQLQGVVSWGYG-CAQRNKPGVYTKVCNYRSWISSTMSSN 238
                                                                                                                                                                                                                                                                                                    201 SSKGA-DICQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 ATLNSRVSAIALPKSCPAAGTQCLISGWGNTQSIGQNYPDVLQCLKAPILSDSVCRNAYP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 ASLGSKVKPISLADHCTQPGGKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYP 189
                                                                                                                                         63 VRLGEHNIAVNEGTEQFIDSVKVIMHPSYNSRNL-D-N-DIMLIKLSKPASLNSYVSTVA 119
                                                                                         4 AFAAPIDDEDDKIVGGYECRKNSASYQASLQSGYHF-CGGSLISSTWVVSAAHCYKSRIQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTFIFLALLGAT-VAFPIDDDDKIVGGYTCSRNSVPYQVSLNSGYHF-CGGSLINSQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 KTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Canis lupus familiaris #common_name dog
30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change
18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQISSNAMCLGYMEGGKDSCQGDSGGPVVCNGELQGVVSWGAG-CAQKGKPGVSPKVCKY
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9
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trypsin (EC 3.4.21.4) precursor, cationic - dog
cationic trypsinogen
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Pred. No. 8.52e-161;
58; Mismatches 80; Indels
   Length 238;
                                  68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #disulfide_bonds #status predicted\
Score 804; DB 2; L
                                  56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -246 ##label PIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.9%;
Best Local Similarity 42.2%;
Matches 106; Conservative
h
Similarity 45.8%;
110; Conservative
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0-160,48-64,
32-233,139-206,
171-185
                                    110;
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Query Match
Best Local S.
Matches 11
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#authors
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24-246
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#journal J. Mol. Biol. (1975) 98:693-717
#title The refined crystal structure of bovine beta-trypsin at 1.8
#cross-references MID:76072097
#contents annotation; X-ray crystallography; binding sites for calcium, substrate, and inhibitors
MENT Trypsinogen is synthesized in the acinar cells of the pancreas.
MENT Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal hexapeptide. Subsequent cleavage after Lys-131 leads to alpha-trypsin. Further cleavage after Lys-176
Lys-131 leads to alpha-trypsin. Further cleavage after Lys-176
SSIFICATION #superfamily trypsin, A cleavage may also occur after Arg-105.
WORDS hydrolase; pancreas; protein digestion; serine proteinase;
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#cleavage_site Lys-ile (enteropeptidase) #status
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#domain activation peptide #status experimental #label
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190 GQITDGMYCAGSSKGA-DTCQGDSGGPLYCDGALQGITSWGSDPCGRSDKPGYYTNICRY 248
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                                                                                                                                                                                                                                                                                                                        #formal_name Bos primigenius taurus #common_name cattle 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change
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#active_site His, Asp, Ser #status experimental\
#binding_site calcium (Glu, Asn, Val, Glu) #status
experimental\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
#journal Biochem. Blophys. Res. Commun. (1966) 24:346-352
#title Covalent structure of bovine trypsinogen. The position remaining amides.
#cross-references MUID:67168848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cession n.v.v.
##molecule_type protein
##residues 1-57,′Q′,59-67,′Q′,69-150,′N′,152-176,′N′,178-229
##label MIK
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th 229 #molecular-weight 23993 #checksum
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                                                                                                                                                                                                                                     TRBOTR #type complete trypsin (EC 3.4.21.4) precursor - bovine
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Amino acid sequence of dogfish trypsin.
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Pred. No. 2.43e-158;
50; Mismatches 68;
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annotation; revisions
the sequence agrees with that shown
A92954
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A90164
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Philos. Trans. R. Soc.
annotation; revisions
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Best Local Similarity 46.6%;
Matches 108; Conservative
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                                                                      NVVEGNEQFISASKSIVHPSYNSNTL-N-N-DIMLIKLKSAASLNSRVASISLPTSCASA 118
                                                                                                                                         GTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SAAHCYKSRIQVRLGEHNIDVVEGGEQFIDAAKIIRHPSYNANTF-D-N-DIMLIKLNSP 117
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        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trypsin (EC 3.4.21.4) precursor, cationic - rat #formal_name Rattus norvegicus #common_name Norway rat 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change A27547
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#binding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 247 #molecular-weight 26269 #checksum 9664
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                                                                                        DDDKIVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNI
                          39 QEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSL
                                                                                                                                                                         149 GQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGSSKGA-DT
                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C. #journal Blochemistry (1987) 26:3081-3086
#title Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
#cross-references WuID:87271609
#accession A27547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-247 ##label FLE ##cross-references GB:M16624; NID:g206498; PID:g206499 FICATION #superfamily trypsin; trypsin homology calcium binding; hydrolase; protein digestion; serine
                                                                                                                                                                                                                          208 CQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVTINICRYLDWIKKIIGSK 259
                                                                                                                                                                                                            CQGDSGGPVVCSGKLQGIVSWGSG-CAQKNKPGVYTKVCNYVSWIKQTIASN 229
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Pred. No. 7.53e-158;
55; Mismatches 82; Indels
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LDWIKKIIGSK 259
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133-234,140-207,
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76,78,81,86
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RESULT

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#domain signal sequence #status predicted #label SIG\
#domain activation peptide #status predicted #label APT\
#product trypsin II #status predicted #label ENZ\
#domain trypsin homology #label TRY\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                     C.; MacDonald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily trypsin; trypsin homology
hydrolase; pancreas; protein digestion; serine proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17GSZ #type complete
trypsin (EC 3.4.21.4) precursor (with pancreatic secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsin (EC 3.4.21.4) II precursor - rat trypsinogen II trypsinogen II trypsinogen II #formal_name Rattus norvegicus #common_name Norway rat 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #active_site His, Asp, Ser #status predicted\
#binding_site calcium (Glu, Asn, Val, Glu) #status
                                                                                                                                                                                                                                                                                                                                                                                                        #authors MacDonald, R.J.; Stary, S.J.; Swift, G.H.
#journal J. Biol. Chem. (1982) 257:9724-9732
#title Two similar but nonallelic rat pancreatic trypsinogens.
#cross-references MUID:82265624
                                                                                                                                                                                              #authors Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacD
R.J.; Rutter, W.J.
#journal J. Biol. Chem. (1984) 259:14255-14264
#title Structure of two related rat pancreatic trypsin genes.
#cross-references_MUID:85054880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 VKLNARVATVALPSSCAPAGTQCLISGWGNTLSSGVNEPDLLQCLDAPLLPQADCEASYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
#length 246 #molecular-weight 26243 #checksum 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sidues 9-246 ##label MAC
The trypsin II mRNA is present in much lower quantities
trypsin I mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #disulfide_bonds #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 781; DB 1; Le
Pred. No. 2.33e-157;
                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-246 ##label CRA
SNCE A00948
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Best Local Similarity 42.6%;
Matches 107; Conservative
                                                                                                                                                     A22657; A00949
A22657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
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75,77,80,85
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24-239
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                                                                                                Marquart, M.; Papamokos, E.; Huber, R. submitted to the Brookhaven Protein Data Bank, September 1982 cross-references PDB:1TGS
                                                                                                                                                                            Bolognesi, M.; Gatti, G.; Menegatti, E.; Guarneri, M.;
Marquart, M.; Papamokos, E.; Huber, R.
J. Mol. Biol. (1982) 162:839
Three-dimensional structure of the complex between pancreatic secretory inhibitor (*azal type) and trypsinogen at 1.8
angstroms resolution. structure solution, orystallographic refinement and preliminary structural interpretation.
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9
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#region helix (right hand 3-10) (contiguous with h3)\
#region helix (right hand alpha) (contiguous with h3)\
#disulfide_bonds\
#disulfide_bonds\
#disulfide_bonds\
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The geometry of the reactive site and of the peptide groups in trypsin, trypsinogen and its complexes with inhibitors. Dayhoff, M.O.
                                                                                                                                                                                                                                                                                                                                          Marquart, M.; Walter, J.; Deisenhofer, J.; Bode, W.; Huber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Atlas of Protein Sequence and Structure (Data Section), Dayhoff, M.O., ed., vol. 5, pp.105, National Biomedical Research Foundation, Silver Spring, Md., 1972
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trypsin inhibitor), chain Z - bovine #formal_name Bos primigenius taurus #common_name cattle
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                                                                                Guarneri, M.;
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                                         pancreas
A50955
Bolognesi, M.; Gatti, G.; Menegatti, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination: X-ray diffraction hydrolase; serine proteinase
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FEATURE
146-158
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216-225
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118-185
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2TLDE #type complete trypsin (EC 3.4.21.4) (with mutant streptomyces subtilisin

TITLE

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#region beta sheet\
#region helix (right hand alpha) (single alpha turn,rest
                                                             #authors Mitsui, Y.; Takeuchi, Y.; Nonaka, T.; Nakamura, K.T.
#submission submitted to the Brookhaven Protein Data Bank, September 1991
#cross-references PDB:2TLD
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Mucleic Acids Res. (1986) 14:8307-8330
Sequence organisation and transcriptional regulation of the mouse elastase II and trypsin genes.
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hand alpha) (contiguous with h2)\
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                                                                                                                                                                                                                                                                                              Takerchi, Y.; Satow, Y.; Nakamura, K.T.; Mitsui, Y. J. Mol. Biol. (1991) 221:309
Refined crystal structure of the complex of subtilisin Bi and streptomyces subtilisin inhibitor at 1.8 angstroms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 VLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKD 92
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trypsin (EC 3.4.21.4) precursor - mouse
#formal_name Mus musculus #common_name house mouse
30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
20-Mar-1998
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Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4407
Crystal structure of an engineered subtilisin inhibitor
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inhibitor), chain E - bovine
#formal_name Bos primigenius taurus #common_name
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#active_site Asp, His, Ser #label CAT\
#site #label 13
#length 223 #molecular-weight 23071 #checksum
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Pred. No. 3.60e-154;
48; Mismatches 68;
                                                                                                                                                                                                                                          complexed with bovine trypsin. TN005551
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#region helix (right
#region helix (right
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Best Local Similarity 46.5%;
Matches 106; Conservative
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179-183,186-193,
204-209,159-163
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7-137,25-41,
109-210,116-183,
148-162,173-197
84,40,177
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46-50,63-67
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116-183
148-162
173-197
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#product trypsin #status predicted #label MAT\
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#blnding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 246 #molecular-weight 26203 #checksum 5833
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trypsin (EC 3.4.21.4) I precursor - rat
trypsinogen I
#formal_name Rattus norvegicus #common_name Norway rat
17-bec-1882 #sequence_revision 17-bec-1882 #text_change
20-Mar-1998
B22657; A00948
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#journal J. Biol. Chem. (1982) 257:9724-9732
#title Two similar but nonallelic rat pancreatic trypsinogens.
Nucleotide sequences of the cloned cDNAs.
#cross-references NUD:82265624
#accession A00948
                         ##monlecule_type mRNA
##residues 1-246 ##label STE
##cross-references GB:X04574; NID:954918; PID:954919
##Cross-references GB:X04574; NID:954918; PID:954919
IFICATION #superfamily trypsin, trypsin homology
RDS calcium binding; hydrolase; protein digestion; serine
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#title Structure of two related rat pancreatic trypsin genes.
#across-references MUID:85054880
#accession B22657
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Pred. No. 3.60e-154;
56; Mismatches 79; Indels
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##cross-references GB:J00778; NID:9206508; ##note the codon ATC for
##note Leu and GAC for residue 170 as Asn
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#cross-references MUID:87066713
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bt Local Similarity 42.7%;
tches 106; Conservative
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#domain signal sequence #status predicted #label SIG\
#domain activation peptide #status predicted #label APT\
#product trypsin I #status predicted #label ENZ\
#domain trypsin homology #label TRY\
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#submission submitted to the Brookhaven Protein Data Bank, September 1994
#cross-references PDB:1TPS
ERENCE TN023754
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#region helix (right hand 3-10) (contiguous with h3)\
#region helix (right hand alpha) (contiguous with h2)\
#disulfide_bonds\
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                                                 14/1; 67/2; 152/1; 197/3
#superfamily trypsin; trypsin homology
hydrolase; pancreas; protein digestion; serine proteinase;
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#active_site His, Asp, Ser #status predicted\
#binding_site calcium (Glu, Asn, Val, Glu) #status
predicted
#length 246 #molecular-weight 25959 #checksum 6732
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Trypsin complexed with inhibitor a90720a - bovine
#formal_name Bos primigenius taurus #common_name
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Pred. No. 6.33e-154;
56; Mismatches 80; Indels
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Determination: X-ray diffraction
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1-246 ##label MAC
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Best Local Similarity 42.3%;
Matches 105; Conservative
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September 1994
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#region helix (right hand 3-10) (contiguous with h3)\
#region helix (right hand alpha) (contiguous with h2)\
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J. Am. Chem. Soc. (1993) 115:12619
Atomic structure of the trypsin-cyclotheonamide a complex: lessons for the design of serine protease inhibitors.
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#formal_name Bos primigenius taurus #common_name cattle
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Score 766; DB 5; Leus ...
Pred. No. 1.11e-153;
''....atches 68; Indels
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Determination: X-ray diffraction
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                Query Match 39.4%;
Best Local Similarity 46.5%;
Matches 106; Conservative
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173-197
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7-137
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Search completed: Wed Jul 22 15:28:54 1998 Job time: 73 secs.

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#authors Kurinov, I.V.; Harrison, R.W.
#submission submitted to the Brookhaven Protein Data Bank, February 1996
#cross-references PDB:1JRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GNEQFISASKSIVHPSYNSNTL-N-N-DIMLIKLKSAASLNSRVASISLPTSCASAGTQC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 LISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 VLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAACKKPYTVRLGDHSLQNKD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVE 59
                                                                                                                                                                                                                                                                                        digestion; hydrolase; pancreas; serine protease; zymogen
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#disulfide_bonds\
#disulfide_bonds
#length 2233 #molecular-weight 23305 #checksum 7159
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1JRTA #type complete
trypsin (EC 3.4.21.4), chain A - bovine
hemiacetal complex between leupeptin and trypsin
                                                                                                                                                                     Kurinov, I.V.; Harrison, R.W.
Nat. Struct. Biol. (1994) 1:735
Prediction of new serine proteinase inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 223;
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Pred. No. 1.11e-153;
48; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 SGGPVVCSGKLQGIVSWGSG-CAQKNKPGVYTKVCNYVSWIKQTIASN 223
                                              #formal_name Bos taurus: #common_name bovine A65928
                                                                                                                                                                                                                                                                                                                             #region helix (right hand 3-10)\
#region helix (right hand alpha)\
#region helix (right hand 3-10)\
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Determination: X-ray diffraction
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Best Local Similarity 46.5%;
Matches 106; Conservative
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209-211
63-66,47-50,15-19,
23-31,34-37,86-90,
67-72
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180-183,186-193,
204-208,160-163
                                                                                                               #submission
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#journal
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#authors
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116-183
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173-197
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                                  PDB_TITLE
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                                                      ORGANISM
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 15.26 Seconds 717.292 Million cell updates/sec Wed Jul 22 15:29:54 1998;

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

not generated. abular output >US-08-915-659A-7 (1-260) from US08915659A.pep 1943 Title: Description: Perfect Score:

Sequence:

1 MGRPRPRAAKTWMFLLLLGG.......VYTNICRYLDWIKKIIGSKG 260

PAM 150 Gap 11 Scoring table:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb15 Database:

1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

scale 0.712 Variance 59.229; Mean 42.195; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2.06e-181 1.55e-180 1.17e-179 1.17e-179 2.30e-179 7.44e-176 1.12e-167 1.23e-165 5.14e-165 5.34e-154 7.73e-153 1.73e-154 0.00e+00 1.15e-206 9.53e-134 6.97e-133 5.59e-187 Pred. No. SERINE PROTESEE INHIBI
PROTEASE M PRECURSOR.
URS1-WORAL BITHELLAL
TRYPSIN ORD (EC
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TISSUE KALLIKREIN.
TRYPSINOGEN B2 PRECURS
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TRYPSINOGEN B2 PRECURS
TRYPSINOGEN B1 PRECURSOR
KALLIKREIN PRECURSOR
KALLIKREIN PRECURSOR
KALLIKREIN (FRAGMENT). CALOBIN. SERINE PROTEASE PRECUR TRYPSINOGEN I (FRAGMEN VENOM PLASMINOGEN ACTI Description 061955 092876 092876 0920920 091515 042158 042158 042159 042160 042159 028773 028774 063275 Q91516 Q91053 O13060 Query Match Length DB Score Š Š Result

241 VYTKICRYTTWIKKTMDNR 259

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2.72e-130 1.02e-129	7.46e-129 3.96e-127	49e-1	1.08e-125	2.94e-124	2.13e-123	5.79e-122	5.86e-120	5.86e-120	5.90e-118	н	8.16e-113	4.23e-113	3.03e-112	1.11e-109	2.94e-108	1.09e-107	1.91e-101	2.58e-100	2.58e-100	1.82e-99	~	on .
SERINE PROTEASE PRECUR	GLANDULAR KALLIKREIN (CAPILLARY PERMEABILITY	റ	MUCOFIRASE 3.	SERINE PROTEASE PRECUR	SERINE PROTEASE PRECUR	MUCOFIRASE 1.	MUCOFIRASE 2.	PREPROTRIMUBIN PRECURS	MUCOFIRASE 4.	MUCOFIRASE 5.	SERINE PROTEASE PRECUR	GRANZYME K.	KN-BJ2 PRECURSOR.	PRECURSOR ADIPSIN.	NATURAL KILLER CELL PR	SERINE PROTEASE PRECUR	GRANZYME-LIKE PROTEIN	LYMPHOCTYE MET-ASE 1 P	CHYMOTRYPSIN BI (FRAGM	NERVE GROWTH FACTOR, G	SERINE PROTEASE HOMOLO	HGF ACTIVATOR LIKE PRO
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ALIGNMENTS

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AC 090
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57 SAAHCYKSRVEVRMGEHHIRVTEGKEQFISSSRVIRHPNYSSYNI-D-N-DIMLIKLSKP 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 GMITDAMFCAGYLQGGKDSCQGDSGGPVVCNGELQGVVSWGYG-CAERDHPGVYAKVCLF 231
                                                                                                                                                                                                                                                                                                                                                                                                  EQLRRITRSVVHPKYHQGSGPILPRRIDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQ 226
                                                                                                                                                                                                                                                                                                                     49 GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWA-RVGDDHLLLLQG- 106
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TISSUE-PYLORIC CAECA;
GENICOT S., RENTIER-DELRUE F., EDWARDS D., VAN BEEUMEN J., GERDAY
BIOCHIM. BIOPHYS. ACTA 1298:45-57(1996).
EMBL; X82223; G559508; -.
SIGNAL; HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARANOTOTHENIA MAGELLANICA.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
ACTINOPTERYGII; PERCIFORMES; NOTOTHENIOIDEI; NOTOTHENIIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 757; DB 12; Length 242;
Pred. No. 2.06e-181;
62; Mismatches 63; Indels 11;
                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                      Score 776; DB 2; Length 273;
Pred. No. 5.59e-187;
46; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST AND SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST AND TATION UPDATE)
TRYPSIN PRECURSOR (EC 3.4.21.4) (ALPHA- AND BETA-TRYPSIN).
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CHAIN 14 242 PROTRYPSIN.
SEQUENCE 242 AA; 26201 MW; DDD27DCA CRC32;
                                                                                                                                                                                             29780 MW; 83E4135C CRC32;
                                                                                                                                         WATANABE K., BAND V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                 SEQUENCE FROM N.A.
MEDLLINE, 96320486.
LIU X.L., WAZER D.E., WATANABE
CANCER RES. 56:3371-3379(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity 46.7%;
Matches 106; Conservative
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Best Local Similarity 44.3%;
Matches 108; Conservative
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SEQUENCE 273 AA; 2978
                  HOMO SAPIENS (HUMAN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 PAKLSELIQPLÞLERDCSANTTSCHILGWGK-TAD-GDFPDTIQCAYIHLVSREECEHAY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LTAAHCKKPNLQVFLGKHNLRQRESSQEQSSVVRAVIHPDYDAAS---HDQDIMLLRLAR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 KTWMFLL-LLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KKLMVVLSLIAAAWA-E--EQNKLVHGGP-CDKTSHPYQAALYTSGHLLCGGVLIHPLWV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                          YAMASHIRO K., TSURUOKA N., KODAMA S., TSUJIMOTO M., YAMAMURA Y.,
TANAKA T., NAKAZATO H., YAMAGUCHI N.;
BIOCHIM. BIOPHYS. ACTA 1350:11-14(1997).
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Pred. No. 1.15e-206;
55; Mismatches 68; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-ALZHERHER'S DISEASE BRAIN TISSUE;
LITTLE S.P., JOHNSTONE E.M., DIXON E.P., NORRIS F., BUCKLEY W.,
BECKER G., JOHNSON M., DOBBINS J.R., WYRICK T., MILLER J.R.,
MACKELLAR W., HEPBURN D., CORVALAN J., MCCLURE D., LIU X.,
STEPHENSON D., CLEMENS J.;
J. BIOL. CHEM. 0:0-0(1997).
EMBL: D78203; G185493; -.
EMBL: D78203; G185493; -.
EMBL: AF013988; G2318115; -.
                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA, MARTAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
ANISOWICZ A., SOTIROPOULOU G., STENMAN G., MOK S.C., SAGER
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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O99920

O99920

O1-MAY-1997 (TREMBLREL. 03, CREATED)

O1-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

NES1-NORMAL EPITHELIAL CELL SPECIFIC GENE 1.
                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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OCFCEFCE CRC32;
                                                                                                     244 AA
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                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 PC
244 PE
26856 MW;
    241 VYTNICRYLDWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.8%;
Matches 118; Conservative
                                                                                                     PRELIMINARY;
                                                                                                                                       01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 YTNWIQKTIQAK 244
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248 YLDWIKKIIGSK 259
                                                                                                                                                                                                       PROTEASE M PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 AA;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-COLON;
MEDLINE; 97157069.
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
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Local Similarity 42.4%;
Local Similarity 42.4%;
Local Similarity 42.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 TNICRYLDWIKKIIG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 DWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AWIAQTIAAN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE KALLIKREIN.
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042608
042608;
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Q61855;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 QPVALPSSCAAAGTMCKVSGWGNTMSSTAD-RNKLQCLNIPILSDRDCENSYPGMITDAM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FCAGYLEGGKDSCQGDSGGPVVCNNELQGVVSWGYG-CAERDHPGVYAKVCLFNDWLEST 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LIAAAYAA-PIDEDDKIVGGYECRKNSVAYQVSLNSGYHF-CGGSLVNENWVVSAAHCYK 58
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                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREE. 01, LAST ANNOTATION UPDATE)
TRYPESINGEN (FRAGMENT).
FUGU RUBRIPES (JAPANESE PUFFERFISH).
EUGARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; TETRAODONTIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٠<u>.</u>
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Pred. No. 1.17e-179;
59; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WANG K., GAN L., LEE I., ROACH J., HOOD L.;
SUBMITIED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U25747; G971196; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011898; G2367495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRYPSINOGEN A2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 754; DB 12; I
Pred. No. 1.55e-180;
64; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D049AA4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 AA; 25726 MW; 6A296989 CRC32;
                                                                                                                                                                                                                    237 AA
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                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.8%;
Best Local Similarity 42.4%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.7%;
Best Local Similarity 42.0%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
232 NDWL 235
                                                                   249 LDWI 252
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IGS 258
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Q91515;
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042158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 LRLKKPADITDVVKPIDLPTEEPKLGSTCLASGWGSITPVKYEYPDELQCVNLKLLPNED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 CAKAHIEKVTDDMLCAGDMDGGKDTCAGDSGGPLICDGVLQGITSWGPSPCGKPNVPGIY 243
                                                                                                                                                                                                                                                        63 HCYQTASRISVRIGEHNIFVNEGTEQQIQASKAIQHPQYNSWTI-D-N-DIMLIKLSSPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 TLNQYAQAIALPSSCVNTGVMCTISGWGETQTSIGS-PDVLMCVQAPVLSDTSCRNSYPG 178
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                                                       179 DITNNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWGRG-CALPNYPGVYTKVCNYN 237
      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
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Pred. No. 1.17e-179;
57; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AA.
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177 DITUNNAICLGYLEGGKDSCQGDSGGPVVCNGQLQGIVSWGRG-CALPNYPGVYTKVCNYN 235
                                                                                                                                              HCYQTASRISVRIGEHNIFVTEGTEQRIQASKAIRHPQYNSATI-D-N-DIMLIKLSSPA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 HCYQTASRISVRIGEHNIFVTEGTEQRIQASKAIRHPQYSSATI.D-N-DIMLIKLSSPA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 738; DB 12; Length 244;
Pred. No. 7.44e-176;
63; Mismatches 74; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011900; G2367499; -.
                                                                                                                                                                                                                                                       LT 10
042159 PRELIMINARY; PRT; 244 AA.
042159; 04.1398 (TREMBLREL 05, CREATED)
01.JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
01.JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
TRYPSINGEN BI PRECURSOR (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                   PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; PISCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25903 MW; 41F78768 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AA.
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AGNATHA (CYCLOSTOMATA).
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244
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                                                                                                                                                                                                                 250 DWIKKIIGSK 259
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250 DWIKKIIGSK 259
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ILNQYAQAIALPSSCVNTGVMCTISGWGETQTSVGS-PDVLMCVQAPVLSDTSCRNSYPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 DITUNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWGRG-CALPNYPGVYTKVCNYN 237
                                                                                                                                                                                                                                                                                                                         4 LILALLVGVAAAAPYMYEDHIVGGSECAAHSQPWQVSLNIGYHF-CGGSLINSQWVVSAA 62
                                                                                                                                                                                                                                                                                                                                            Score 744; DB 12; Length 245;
Pred. No. 1.31e-177;
61; Mismatches 74; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IFALLVGTA-AAAPYMYEDHIVGGYECAAHSQPWQVSLNIGYHF-CGGSLISSEWVVSAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                      Length 247;
                                                                                                                                                                                                                                                                   Score 750; DB 12; Length 247
Pred. No. 2.30e-179;
59; Mismatches 77; Indels
                                                                   ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                    SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011899; G2367497; -.
EMBL; AF011352; G2293478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROACH J.C.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011901; G2367501; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRYPSINOGEN B2 PRECURSOR (FRAGMENT).
PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETROMYZON MARINUS (SEA LAMPREY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
AGNATHA (CYCLOSTOMATA).
                                                                                                                                                                                                                            TRYPSIN A3.
6D71AC2E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
TRYPSIN B2.
071872F0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 AA
                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
13 PO
245 TR
26001 MW;
                                                                                                                                                                                                                                         26295 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                   Jery Match 38.6%; st Local Similarity 42.0%; atches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 38.3%;
Local Similarity 42.0%;
Les 105; Conservative
                                                                                                             SEQUENCE FROM N.A.
TISSUE-ANTERIOR INTESTINE;
                           AGNATHA (CYCLOSTOMATA).
                                                                                                                                                                                                              15
247
                                                                                                                                                                                                              1
16 2
247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AWIAQTIAAN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 DWIKKIIGSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 AA;
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777
                                                                                                                                          ROACH J.C.;
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    042160
042160,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SIGNAL
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RESULT

Matches

Gaps 10;

59

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AVFVRVLSYVKWIEDTIAENS
                                     240 GVYTNICRYLDWIKKIIGSKG
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        <sub>2</sub>2
                                                                                                                                                                                                                                              STRAIN-MONGREL;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                  029474;
                                                                           JT 13
Q29474
                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
           238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 ONKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMLLRLTQPAEITDAVQVVELPTQEPEVGSTCLASGWGSIEPENFSYPDDLQCVDLKILP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IMLLOLRDOASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDKCAKAHTQKVTEFMLCAGHLEGGKDTCVGDSGGPLTCDGVLQGVTSWGYIPCGSPNKP 237
                                                                                                                                                                                                                                          91 KVLEGNEQFINAAKIIRHPKYNR-DTLD-N-DIMLIKLSSPAVINARVSTISLPTAPPAA 147
                                                                                                                                                                                                                                                                                             148 GTECLISGWGNTLSFGADYPDELKCLDAPVLTQAECKASYPGKITNSMFCVGFLEGGKDS 207
                                                                                                                                                                                                                                                                                                                     149 GOKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMYCAGSSKGA-DT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTAAHCIGDNYQLWLGRHNLFDDEDTAQFVHVSESFPHPCFNMSLLKNHTRQADEDYSHD 117
                                                                                                                                                                                                        29 QEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKFKYTVRLGDHSL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79; Indels 16; Gaps
                                                                                                                                                                                         33 DDDKIVGGYTCE-NSLPYQVSLNSGSHF-CGGSLISEQWVVSAAHCYKTRIQVRLGEHNI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 WFLVLCLALSLGG-TGAAPPIQSRIVGGWEC---SQPWQAALYHFSTFQCGGILVHPQWV 57
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 WMFLL-L-LG-GAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWV
                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                               208 CQRDSGGPVVCNGQLQGVVSWGHG-CAWKNRPGVYTKVYNYVDWIKDTIAANS 259
                                                                                                                                                                                                                                                                                                                                                              ealio hamadryas (hamadryas baboon).
Eukrakota, metazoa, chordata, vertebrata, tetrapoda, mammalia,
Eutheria, primates.
CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
                                                                                                                                       Length 259
                                                                           æ,
                                                                                                                                                   Pred. No. 1.12e-167;
51; Mismatches 77; Indels
                                                                         WIEGAND U., CORBACH S., MINN A., KANG J., MUELLER-HILL GENE 136:167-175(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERELYGINA L.M., KAMMERER C.M., HENKEL R.D.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L43121; G871814; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.23e-165;
57; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE KALLIKREIN.
OC5E883F CRC32;
                                                                                                              27983 MW; D2F07A3E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                        Score 710;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28339 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Journy Match
Best Local Similarity 41.8%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLK1.
PAPIO HAMADRYAS (HAMADRYAS
                                                                                                                                       Query Match
Best Local Similarity 42.1%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL; SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
KALLIKREIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258
                                                                                                EMBL; X71345; E74009;
SEQUENCE 259 AA; 2
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 25 ; SEQUENCE 258 AA;
                                                                                                               259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                   FROM N.A.
                                                             MEDLINE; 94123994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=PANCREAS;
                                                  TISSUE-BRAIN;
EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      028773;
                                                                                                                                                                                                                                                                                                                                                                                                              T 12
Q28773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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SETTOS

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MEDLINE; 94250683.

MEDLINE; 94250683.

GAUTHIER E.R., DUMAS C., CHAPDELAINE P., TREMBLAY R.R., DUBE J.Y.;
BIOCHIM. BIOPHYS. ACTA 1218:102-104(1994).

-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-|-XAA BONDS IN SWALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE RALLIDIN (LYSYL-BRADYKININ) FROM KININOGENS HYDOLYSES HYDOLYSIS OF MET-|-XAA OR LEU-|-XAA THE RAY ENZYME IS UNUGUAL IN LIBERALING' BRADYKININ DIRECTLY FROM AUTOLOGOUS KININOGENS BY CLEAVAGE AT TWO ARG-|-XAA BONDS.

EMBL; X75479; 6414019; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TAAHCINDNYQLWLGRYNLFEHEDTAQFVQVRESFPHPEFNLSLLKNHTRLPEEDYSHDI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 MLLRLAEPAQITDAVRVLDLPTQEPQVGSTCYASGWGSIEPDKFIYPDDLQCVDLELLSN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 DICANAHSQKVTEFMLCAGHLEGGKDTCVGDSGGPLICDGVLQGITSWGHVPCGSPNMPA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 WFLVLCLALSLAGTGAAPPVQSRIIGGWDCTKNSQPWQAALYHYSKFQCGGVLVHPEWVV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                               01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLEEL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLEEL. 05, LAST ANNOTATION UPDATE)
KALLIKREIN PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (GLANDULAR KALLIKREIN) (KININOGENIN).
CANIS FAMILIARIS (DOG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAPODA; MAMMALIA;
                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 703; DB 4; Length 261; 40.2%; Pred. No. 1.23e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALLIKREIN.
65B49AEF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALLIKREIN (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 K
28913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 VYTKVISHLEWIKETMTAN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01,
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 40.2%;
es 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 PRELIMINAR Q63275 C82375 C92375 C92375 C92707-1996 (TREMBLREL. 0 01-NOV-1996 (TREMBLREL. 0 01-NOV-1996 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VYTNICRYLDWIKKIIGSK
                                                                                                                                                                                                                      EUTHERIA; CARNIVORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; RODENTIA
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Score 694; DB 10; Length 239;
Pred. No. 5.14e-163;
52; Mismatches 63; Indels 15; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                    121 TKEPKVGSTCLVSGWGS-TNPSEWEFPDDLQCVNIHLLSNEKCIKAYKEKVTDLMLCAGE 179
                                                                                                                                                                                                                                              63 SEDV-QHRL-VSQSFRHPDYKPFLMRNHTRKPKDYSNDLMLLHLSEPADITDGVKVIDLP 120
                                                                                                                                                                                                                                                                                                                                  143 DHCTQPGQKCTVSGWGTVTSPRE-NFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 WYNPYSMQVILGDHNLRVFEGTEQLMKTNTIIWHPSYDYQTL-DF--DIMLIKLYHPVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TEAVAPIPLPTSCPYGGLSCSVSGWGIAKLGGEAYMPTLLQCLNVPIVDQQVCENTYPGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISTIMVCAGYMEGGKDACNGDSGSPLVCDGEVQGLVSWG-QGCAEPNYPGVYVKLCEFHS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 EDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQ 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LLLLIGAAAAVPR-EDGRIIGGYECSPHSRPYMASLNYGYHF-CGGVLINNQWYLSVAHC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEN L., DEVRIES A.L., CHENG C.H.;
PROC. NATL. ACAD. SCI. U.S.A. 94:3811-3816(1997).
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-XAA, LYS-|-XAA, EMBL; U58845; G1399811;
-: EMBL; U58835; G2102686; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 34.1%; Score 663; DB 12; Length 249; Local Similarity 41.8%; Pred. No. 5.33e-154; hes 104; Conservative 49; Mismatches 86; Indels 10; Gaps
                                                                                                                                                                            6 QSRVVGGFKCEKNSQPWQVAVIN-EDL-CGGVLIDPSWVITAAHCYSDNYHVLLGQNNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 15
92046
92046
032046; O13261;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PREPROTRYPSIN PRECURSOR (EC 3.4.21.4) (ALPHA- AND BETA-TRYPSIN).
DISSOSTICHUS MAWSONI.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES; NOTOTHENIOIDEI; NOTOTHENIDAE.
                                                                                                                                                                                                                                                                                                                                                                                  180 LEGGKDTCRGDSGGPLICDGVLQGITSWGSVPCGEPNKPGIYTKLIKFTSWIKEVM 235
                                                                                                                                                                                                                                                                                                                                                                                                      102 SKGA-DTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDMIKKII 256
ZINTZ C.B., MA J.X., CHAO J., CHAO L.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L33840; G609585; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PANCREAS;
CHEN L., DEVRIES A.L., CHENG C.H.C.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTRYPSIN.
55C59EB4 CRC32;
                                                                     0609E3E6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                 NON TER 1 1
SEQUENCE 239 AA; 26382 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 15 PH
16 249 PH
249 AA; 27169 MW;
                                                                                                    Query Match
Best Local Similarity 44.9%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL; HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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